

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/756,018**

INPUT SET: S18591.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 3 (1) General Information:

4 (i) APPLICANT: Seed, Brian et al.

5 (ii) TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES

6 AND METHODS

7 (iii) NUMBER OF SEQUENCES: 16

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: Clark & Elbing LLP

10 (B) STREET: 585 Commercial Street

11 (C) CITY: Boston

12 (D) STATE: MA

13 (E) COUNTRY: USA

14 (F) ZIP: 02109-1024

15 (v) COMPUTER READABLE FORM:

16 (A) MEDIUM TYPE: Floppy disk

17 (B) COMPUTER: IBM PC compatible

18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (vi) CURRENT APPLICATION DATA:

21 (A) APPLICATION NUMBER: 08/756,018

22 (B) FILING DATE: 25-NOV-96

23 (C) CLASSIFICATION:

24 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: US 08/661,960

26 (B) FILING DATE: 12-JUN-1996

27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: US 60/000,213

29 (B) FILING DATE: 14-JUN-1995

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: Elbing, Karen Lech

32 (B) REGISTRATION NUMBER: 35,238

33 (C) REFERENCE/DOCKET NUMBER: 00786/284002

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 617/723-6777

36 (B) TELEFAX: 617/723-8962

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47 (C) TELEX:

48 49 (2) INFORMATION FOR SEQ ID NO:1:

50 51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 10 amino acids
53 (B) TYPE: amino acid
54 (C) STRANDEDNESS: Not Relevant
55 (D) TOPOLOGY: linear

56 57 (ii) MOLECULE TYPE: protein

58 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60 61 Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
62 1 5 10

63 64 (2) INFORMATION FOR SEQ ID NO:2:

65 66 (i) SEQUENCE CHARACTERISTICS:
67 (A) LENGTH: 18 amino acids
68 (B) TYPE: amino acid
69 (C) STRANDEDNESS: Not Relevant
70 (D) TOPOLOGY: linear

71 72 (ii) MOLECULE TYPE: protein

73 74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

75 76 Met Ala Thr Asn Ser Leu Glu Thr Ser Thr Gly Thr Ser Gly Pro Pro
77 1 5 10 15

78 79 Val Thr

80

81 82 (2) INFORMATION FOR SEQ ID NO:3:

83 84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 42 amino acids
86 (B) TYPE: amino acid
87 (C) STRANDEDNESS: Not Relevant
88 (D) TOPOLOGY: linear

89 90 (ii) MOLECULE TYPE: protein

91 92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

93 94 Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly Pro
95 1 5 10 1596 97 • Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp
98 20 25 30

99

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100	Tyr	Asp	Phe	Leu	Pro	Glu	Thr	Glu	Pro	Pro
101				35				40		

102
103 (2) INFORMATION FOR SEQ ID NO:4:

104 *THE SEQUENCE CHARACTERISTICS:*

105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 20 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS: Not Relevant
109 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

114 Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
115 1 5 10 15
116

117
118 Leu Pro Glu Thr
119 20

120
121 (2) INFORMATION FOR SEQ ID NO:5:
122

122
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 20 amino acids
125 (B) TYPE: amino acid
126 (C) STRANDEDNESS: Not Relevant
127 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

130
131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

132 Arg Asp Arg Arg Gln Ala Thr Glu Phe Glu Phe Leu Asp Phe Asp Phe
133 1 5 10 15
134

135
136 Leu Pro Glu Thr
137 20

139 (2) INFORMATION FOR SEQ ID NO:6:

146 *ALL MOLECULES TYPE: protein*

147 (xi) MOLECULAR FIVE: 4
148
149 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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153 Leu Pro Glu Ala
154 20
155
156

157 (2) INFORMATION FOR SEQ ID NO:7:

158
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 20 amino acids
161 (B) TYPE: amino acid
162 (C) STRANDEDNESS: Not Relevant
163 (D) TOPOLOGY: linear

164
165 (ii) MOLECULE TYPE: protein

166
167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

168 Arg Asp Arg Arg Gln Ala Ala Glu Phe Glu Phe Leu Asp Phe Asp Phe
169 1 5 10 15
170

171 Leu Pro Glu Ala
172 20
173

174 (2) INFORMATION FOR SEQ ID NO:8:

175
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 2287 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: single
180 (D) TOPOLOGY: linear

181
182 (ii) MOLECULE TYPE: DNA (genomic)

183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

186 AAGCTTACCA CCATGGACTG GACCTGGAGG TTCCCTTTCT TTGTGGTGGC AGCAGCTACA	60
187	
188 GGTGTCCAGT CCCAGGTGCA GCTGGTGCAG TCTGGGCTG AGGTGAAGAA GCCTGGTCC	120
189	
190 TCGGTGAAGG TCTCCTGCAA GGCTTCTGGA GGCACCTTCA GCAGCTATGC TATCAGCTGG	180
191	
192 GTGCGACAGG CCCCTGGACA AGGGCTTGAG TGGATGGAG GGATCATCCC TATCTTGTT	240
193	
194 ACAGCAAAC ACTGCACAGAA GTTCCAGGGC AGAGTCACGA TTACCGCGGA CGAATCCACG	300
195	
196 AGCACAGCCT ACATGGAGCT GAGCAGCCTG AGATCTGAGG ACACGGCCGT GTATTACTGT	360
197	
198 GCGAGAGATA ATGGAGCGTA TTGTAGTGTT GGTAGCTGCT ACTCGGGCTG GWTGACCCCC	420
199	
200 TGGGGCCAGG GAACCCTGGT CACCGTCTCT TCAGGTGAGT ACTGAATCT AGCTTCTGG	480
201	
202 GGCAGGCCAG GCCTGACCTT GGCTTTGGGG CAGGGAGGGG GCTAAGGTGA GGCAGGTGGC	540
203	
204 GCCAGCAGGT GCACACCCAA TGCCCATGAG CCCAGACACT GGACGCTGAA CCTCGCGGAC	600
205	

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206 AGTTAAGAAC CCAGGGGCCT CTGCGCCTGG GCCCAGCTCT GTCCCACACC GCGGTACAT 660
207 208 GGCACCAACCT CTCTTGACAGC CTCCACCAAG GGCCCACATCGG TCTTCCCCCT GGCACCCCTCC 720
209 210 TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTACTTCCCC 780
211 212 GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG 840
213 214 GCTGTCCTAC AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC 900
215 216 AGCTTGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG 960
217 218 GACAAGAAAG TTGGTGAGAG GCCAGCACAG GGAGGGAGGG TGTCTGCTGG AAGCAGGCTC 1020
219 220 AGCGCTCCTG CCTGGACCGA TCCCCGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC 1080
221 222 CCCGTCTGCC TCTTCACCCG GAGCCTCTGC CCGCCCCACT CATGCTCAGG GAGAGGGTCT 1140
223 224 TCTGGCTTTT TCCCAGGCTC TGGGCAGGCA CAGGCTAGGT GCCCCTAACCC CAGGCCCTGC 1200
225 226 ACACAAAGGG GCAGGTGCTG GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCCTGC 1260
227 228 CCCTGACCTA AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1320
229 230 CTCCTCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCCA GAGCCCAAAT CTTGTGACAA 1380
231 232 AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCCAG GCCTCGCCCT CCAGCTCAAG 1440
233 234 GCGGGACAGG TGCCCTAGAG TAGCCTGCAT CCAGGGACAG GCCCCAGCCG GGTGCTGACA 1500
235 236 CGTCCACCTC CATCTCTTCC TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCCT 1560
237 238 TCCCCCAAA ACCCAAGGAC ACCCTCATGA TCTCCCGAC CCCTGAGGTC ACATGCGTGG 1620
239 240 TGGTGGACGT GAGCCACGAA GACCTTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG 1680
241 242 AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGGGTGG 1740
243 244 TCAGCGTCCT CACCGTCCTG CACCAAGACT GGCTGAATGG CAAGGAGTAC AAGTGCAGG 1800
245 246 TCTCCAACAA AGCCCTCCCA GCCCCCCATCG AGAAAACCCT CTCCAAAGCC AAAGGTGGGA 1860
247 248 CCCGTGGGGT GCGAGGGCCA CATGGACAGA GGCGGGCTCG GCCCACCCCTC TGCCCTGAGA 1920
249 250 GTGACCGCTG TACCAACCTC TGTCCTACAG GGCAGCCCCG AGAACCCACAG GTGTACACCC 1980
251 252 TGCCCCCATT CCGGGATGAG CTGACCAAGA ACCAGGTCAAG CCTGACCTGC CTGGTCAAAG 2040
253 254 GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT 2100
255 256 ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA 2160
257 258

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SEQUENCE VERIFICATION REPORT
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